

Docket No. 1110-0307P

submitted herewith in full compliance to 37 C.F.R. §§1.821-1.825 is a disk copy of the Substitute Sequence Listing. The disk copy of the Substitute Sequence Listing, file "2002-12-06 1110-0307P.txt", is identical to the paper copy, except that it lacks formatting.

The amendment to the Specification is being made to replace the Sequence Listing as filed with the enclosed substitute Sequence Listing, which is compliant with the USPTO sequence requirements. No new matter is introduced by this amendment.

If necessary, the Commissioner is hereby authorized in this, concurrent, and future replies, to charge payment or credit any overpayment to Deposit Account No. 02-2448 for any additional fees required under 37 C.F.R. § 1.16 or under 37 C.F.R. § 1.17; particularly, extension of time fees.

Respectfully submitted,

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GMM/MAA/CVC
1110-0307P

Attachments: Disk Copy of Sequence Listing
 Paper Copy of Sequence Listing
 Copy of Notice to Comply

(Rev. 03/27/01)

<210> 2
 <211> 127
 <212> PRT
 <213> Mus sp.

<400> 2
 Met Met Ser Ser Ala Gln Phe Leu Gly Leu Leu Leu Leu Cys Phe Gln
 1 5 10 15
 Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser
 20 25 30
 Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp
 35 40 45
 Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val
 50 55 60
 Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser
 65 70 75 80
 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asn Tyr Ser Leu Thr Ile Ser
 85 90 95
 Asn Leu Glu Gln Gly Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Ser
 100 105 110
 Thr Leu Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 115 120 125

<210> 3
 <211> 408
 <212> DNA
 <213> Mus sp.

<220>
 <221> CDS
 <222> (1)..(408)

<400> 3
 atg gat tgg gtg tgg acc ttg cta ttc ctg ata gca gct gcc caa agt 48
 Met Asp Trp Val Trp Thr Leu Leu Phe Leu Ile Ala Ala Ala Gln Ser
 1 5 10 15
 gcc caa gca cag atc cag ttg gtg cag tct gga cct gag ctg aag aag 96
 Ala Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys
 20 25 30
 cct gga gag aca gtc aag atc tcc tgc aag gct tct ggg tat acc ttc 144
 Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45
 aca gaa tat cca atg cac tgg gtg aag cag gct cca gga aag ggt ttc 192
 Thr Glu Tyr Pro Met His Trp Val Lys Gln Ala Pro Gly Lys Gly Phe
 50 55 60
 aag tgg atg ggc atg ata tac acc gac act gga gag cca tca tat gct 240

Lys Trp Met Gly Met Ile Tyr Thr Asp Thr Gly Glu Pro Ser Tyr Ala
 65 70 75 80

gaa gag ttc aag ggg cgg ttt gcc ttc tct ttg gag acc tct gcc agc 288
 Glu Glu Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser
 85 90 95

act gcc tat ttg cag atc aac ttc ctc aaa aat gag gac acg gct aca 336
 Thr Ala Tyr Leu Gln Ile Asn Phe Leu Lys Asn Glu Asp Thr Ala Thr
 100 105 110

tat ttc tgt gta aga ttt tac tgg gat tac ttt gac tac tgg ggc caa 384
 Tyr Phe Cys Val Arg Phe Tyr Trp Asp Tyr Phe Asp Tyr Trp Gly Gln
 115 120 125

ggc acc act ctc aca gtc tcc tca 408
 Gly Thr Thr Leu Thr Val Ser Ser
 130 135

<210> 4
 <211> 136
 <212> PRT
 <213> Mus sp.

<400> 4
 Met Asp Trp Val Trp Thr Leu Leu Phe Leu Ile Ala Ala Ala Gln Ser
 1 5 10 15

Ala Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys
 20 25 30

Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45

Thr Glu Tyr Pro Met His Trp Val Lys Gln Ala Pro Gly Lys Gly Phe
 50 55 60

Lys Trp Met Gly Met Ile Tyr Thr Asp Thr Gly Glu Pro Ser Tyr Ala
 65 70 75 80

Glu Glu Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser
 85 90 95

Thr Ala Tyr Leu Gln Ile Asn Phe Leu Lys Asn Glu Asp Thr Ala Thr
 100 105 110

Tyr Phe Cys Val Arg Phe Tyr Trp Asp Tyr Phe Asp Tyr Trp Gly Gln
 115 120 125

Gly Thr Thr Leu Thr Val Ser Ser
 130 135

<210> 5
 <211> 381
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(381)

<400> 5

atg gag acc gat acc ctc ctg cta tgg gtc ctc ctg cta tgg gtc cca 48
 Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
 1 5 10 15

gga tca acc gga gat att cag atg acc cag agt ccg tcg acc ctc tct 96
 Gly Ser Thr Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser
 20 25 30

gct agc gtc ggg gat agg gtc acc ata act tgc agg gca agt cag gac 144
 Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp
 35 40 45

att tcg aat tat tta aac tgg tat cag cag aag cca ggc aaa gct ccc 192
 Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
 50 55 60

aag ctt cta att tat tac aca tca aga tta cac tca ggg gta cct tca 240
 Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser
 65 70 75 80

cgc ttc agt ggc agt gga tct ggg acc aat tat acc ctc aca atc tcg 288
 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asn Tyr Thr Leu Thr Ile Ser
 85 90 95

agt ctg cag cca gat gat ttc gcc act tat ttt tgc caa cag ggt agt 336
 Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Ser
 100 105 110

acg ctt ccg tgg acg ttc ggt cag ggg acc aag gtg gag gtc aaa 381
 Thr Leu Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys
 115 120 125

<210> 6
 <211> 127
 <212> PRT
 <213> Homo sapiens

<400> 6

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
 1 5 10 15

Gly Ser Thr Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser
 20 25 30

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp
 35 40 45

Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
 50 55 60

Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser
 65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asn Tyr Thr Leu Thr Ile Ser
85 90 95

Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Ser
100 105 110

Thr Leu Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys
115 120 125

<210> 7
<211> 408
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(408)

<400> 7
atg gat tgg gtg tgg acc ttg cta ttc ctg ata gct gca gcc caa agt 48
Met Asp Trp Val Trp Thr Leu Leu Phe Leu Ile Ala Ala Ala Gln Ser
1 5 10 15
gcc caa gca cag gtc cag ttg gtg cag tct gga gct gag gtg aag aag 96
Ala Gln Ala Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30
cct gga agc tca gtc aag gtg tcc tgc aaa gct tct ggg tat acc ttc 144
Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45
aca gaa tat cca atg cac tgg gtg aga cag gct cca gga cag ggt ttc 192
Thr Glu Tyr Pro Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Phe
50 55 60
aag tgg atg ggc atg ata tac acc gac act gga gag cca tca tat gct 240
Lys Trp Met Gly Met Ile Tyr Thr Asp Thr Gly Glu Pro Ser Tyr Ala
65 70 75 80
gaa gag ttc aag gga cgg ttt aca ttc act ttg gac acc tct acc aac 288
Glu Glu Phe Lys Gly Arg Phe Thr Phe Thr Leu Asp Thr Ser Thr Asn
85 90 95
act gcc tat atg gag ctc agc tct ctc agg tct gag gac acg gct gtc 336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
100 105 110
tat tac tgt gta aga ttt tac tgg gat tac ttt gac tac tgg ggt caa 384
Tyr Tyr Cys Val Arg Phe Tyr Trp Asp Tyr Phe Asp Tyr Trp Gly Gln
115 120 125
ggg acc ctg gtc aca gtc tcc tca 408
Gly Thr Leu Val Thr Val Ser Ser
130 135

<210> 8
<211> 136

<212> PRT
<213> Homo sapiens

<400> 8

Met Asp Trp Val Trp Thr Leu Leu Phe Leu Ile Ala Ala Ala Gln Ser
1 5 10 15

Ala Gln Ala Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

Thr Glu Tyr Pro Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Phe
50 55 60

Lys Trp Met Gly Met Ile Tyr Thr Asp Thr Gly Glu Pro Ser Tyr Ala
65 70 75 80

Glu Glu Phe Lys Gly Arg Phe Thr Phe Thr Leu Asp Thr Ser Thr Asn
85 90 95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Val Arg Phe Tyr Trp Asp Tyr Phe Asp Tyr Trp Gly Gln
115 120 125

Gly Thr Leu Val Thr Val Ser Ser
130 135

<210> 9

<211> 1182

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (36)..(1169)

<400> 9

ttttcttcca tttcaggtgt cgtgaggaat tcacc atg ctg ggc atc tgg acc 53
Met Leu Gly Ile Trp Thr
1 5

ctc cta cct ctg gtt ctg act agt gtc gct act cag aac ttg gaa ggc 101
Leu Leu Pro Leu Val Leu Thr Ser Val Ala Thr Gln Asn Leu Glu Gly
10 15 20

ctg cat cat gat ggc caa ttc tgc cat aag ccc tgt cct cca ggt gaa 149
Leu His His Asp Gly Gln Phe Cys His Lys Pro Cys Pro Pro Gly Glu
25 30 35

agg aaa gct agg gac tgc aca gtc aat ggg gat gaa cca gac tgc gtg 197
Arg Lys Ala Arg Asp Cys Thr Val Asn Gly Asp Glu Pro Asp Cys Val
40 45 50

ccc tgc caa gaa ggg aag gag tac aca gac aaa gcc cat ttt tct tcc 245
6

B1
cont

Pro	Cys	Gln	Glu	Gly	Lys	Glu	Tyr	Thr	Asp	Lys	Ala	His	Phe	Ser	Ser		
55					60					65					70		
aaa	tgc	aga	aga	tgt	aga	ttg	tgt	gat	gaa	gga	cat	ggc	tta	gaa	gtg		293
Lys	Cys	Arg	Arg	Cys	Arg	Leu	Cys	Asp	Glu	Gly	His	Gly	Leu	Glu	Val		
				75					80					85			
gaa	ata	aac	tgc	acc	cgg	acc	cag	aat	acc	aag	tgc	aga	tgt	aaa	cca		341
Glu	Ile	Asn	Cys	Thr	Arg	Thr	Gln	Asn	Thr	Lys	Cys	Arg	Cys	Lys	Pro		
			90					95					100				
aac	ttt	ttt	tgt	aac	tct	act	gta	tgt	gaa	cac	tgt	gac	cct	tgc	acc		389
Asn	Phe	Phe	Cys	Asn	Ser	Thr	Val	Cys	Glu	His	Cys	Asp	Pro	Cys	Thr		
		105					110					115					
aaa	tgt	gaa	cat	gga	atc	atc	aag	gaa	tgc	aca	ctc	acc	agc	aac	acc		437
Lys	Cys	Glu	His	Gly	Ile	Ile	Lys	Glu	Cys	Thr	Leu	Thr	Ser	Asn	Thr		
	120				125						130						
aag	tgc	aaa	gag	gaa	gga	tcc	aga	tct	aac	gag	ccc	aaa	tct	tgt	gac		485
Lys	Cys	Lys	Glu	Glu	Gly	Ser	Arg	Ser	Asn	Glu	Pro	Lys	Ser	Cys	Asp		
135					140					145					150		
aaa	act	cac	aca	tgc	cca	ccg	tgc	cca	gca	cct	gaa	ctc	ctg	ggg	gga		533
Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly		
				155					160					165			
ccg	tca	gtc	ttc	ctc	ttc	ccc	cca	aaa	ccc	aag	gac	acc	ctc	atg	atc		581
Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile		
			170					175					180				
tcc	cgg	acc	cct	gag	gtc	aca	tgc	gtg	gtg	gtg	gac	gtg	agc	cac	gaa		629
Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu		
		185					190					195					
gac	cct	gag	gtc	aag	ttc	aac	tgg	tac	gtg	gac	ggc	gtg	gag	gtg	cat		677
Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His		
	200					205					210						
aat	gcc	aag	aca	aag	ccg	cgg	gag	gag	cag	tac	aac	agc	acg	tac	cgt		725
Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg		
215					220					225					230		
gtg	gtc	agc	gtc	ctc	acc	gtc	ctg	cac	cag	gac	tgg	ctg	aat	ggc	aag		773
Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys		
				235					240					245			
gag	tac	aag	tgc	aag	gtc	tcc	aac	aaa	gcc	ctc	cca	gcc	ccc	atc	gag		821
Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu		
			250					255					260				
aaa	acc	atc	tcc	aaa	gcc	aaa	ggg	cag	ccc	cga	gaa	cca	cag	gtg	tac		869
Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr		
		265					270					275					
acc	ctg	ccc	cca	tcc	cgg	gat	gag	ctg	acc	aag	aac	cag	gtc	agc	ctg		917
Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu		
	280					285					290						

B1
cont

acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg 965
 Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 295 300 305 310
 gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc gtg 1013
 Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 315 320 325
 ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac 1061
 Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 330 335 340
 aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat 1109
 Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 345 350 355
 gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct ccg 1157
 Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 360 365 370
 ggt aaa tga tag ggtaccttct gag 1182
 Gly Lys
 375

<210> 10
 <211> 376
 <212> PRT
 <213> Homo sapiens

<400> 10
 Met Leu Gly Ile Trp Thr Leu Leu Pro Leu Val Leu Thr Ser Val Ala
 1 5 10 15
 Thr Gln Asn Leu Glu Gly Leu His His Asp Gly Gln Phe Cys His Lys
 20 25 30
 Pro Cys Pro Pro Gly Glu Arg Lys Ala Arg Asp Cys Thr Val Asn Gly
 35 40 45
 Asp Glu Pro Asp Cys Val Pro Cys Gln Glu Gly Lys Glu Tyr Thr Asp
 50 55 60
 Lys Ala His Phe Ser Ser Lys Cys Arg Arg Cys Arg Leu Cys Asp Glu
 65 70 75 80
 Gly His Gly Leu Glu Val Glu Ile Asn Cys Thr Arg Thr Gln Asn Thr
 85 90 95
 Lys Cys Arg Cys Lys Pro Asn Phe Phe Cys Asn Ser Thr Val Cys Glu
 100 105 110
 His Cys Asp Pro Cys Thr Lys Cys Glu His Gly Ile Ile Lys Glu Cys
 115 120 125
 Thr Leu Thr Ser Asn Thr Lys Cys Lys Glu Glu Gly Ser Arg Ser Asn
 130 135 140
 Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

ctg cta cct ctg gtt ctg act agt gtc gct act cag aac ttg gaa ggc 101
 Leu Leu Pro Leu Val Leu Thr Ser Val Ala Thr Gln Asn Leu Glu Gly
 10 15 20
 ctg cat cat gat ggc caa ttc tgc cat aag ccc tgt cct cca ggt gaa 149
 Leu His His Asp Gly Gln Phe Cys His Lys Pro Cys Pro Pro Gly Glu
 25 30 35
 agg aaa gct agg gac tgc aca gtc aat ggg gat gaa cca gac tgc gtg 197
 Arg Lys Ala Arg Asp Cys Thr Val Asn Gly Asp Glu Pro Asp Cys Val
 40 45 50
 ccc tgc caa gaa ggg aag gag tac aca gac aaa gcc cat ttt tct tcc 245
 Pro Cys Gln Glu Gly Lys Glu Tyr Thr Asp Lys Ala His Phe Ser Ser
 55 60 65 70
 aaa tgc aga aga tgt aga ttg tgt gat gaa gga cat ggc tta gaa gtg 293
 Lys Cys Arg Arg Cys Arg Leu Cys Asp Glu Gly His Gly Leu Glu Val
 75 80 85
 gaa ata aac tgc acc cgg acc cag aat acc aag tgc aga tgt aaa cca 341
 Glu Ile Asn Cys Thr Arg Thr Gln Asn Thr Lys Cys Arg Cys Lys Pro
 90 95 100
 aac ttt ttt tgt aac tct act gta tgt gaa cac tgt gac cct tgc acc 389
 Asn Phe Phe Cys Asn Ser Thr Val Cys Glu His Cys Asp Pro Cys Thr
 105 110 115
 aaa tgt gaa cat gga atc atc aag gaa tgc aca ctc acc agc aac acc 437
 Lys Cys Glu His Gly Ile Ile Lys Glu Cys Thr Leu Thr Ser Asn Thr
 120 125 130
 aag tgc aaa gag gaa gga tcc aga tct aac gag ccc aaa tct tgt gac 485
 Lys Cys Lys Glu Glu Gly Ser Arg Ser Asn Glu Pro Lys Ser Cys Asp
 135 140 145 150
 aaa act cac aca tgc cca ccg tgc cca tag tga ggtaccttct gag 531
 Lys Thr His Thr Cys Pro Pro Cys Pro
 155

<210> 12
 <211> 159
 <212> PRT
 <213> Homo sapiens

<400> 12
 Met Leu Gly Ile Trp Thr Leu Leu Pro Leu Val Leu Thr Ser Val Ala
 1 5 10 15
 Thr Gln Asn Leu Glu Gly Leu His His Asp Gly Gln Phe Cys His Lys
 20 25 30
 Pro Cys Pro Pro Gly Glu Arg Lys Ala Arg Asp Cys Thr Val Asn Gly
 35 40 45
 Asp Glu Pro Asp Cys Val Pro Cys Gln Glu Gly Lys Glu Tyr Thr Asp
 50 55 60

Lys Ala His Phe Ser Ser Lys Cys Arg Arg Cys Arg Leu Cys Asp Glu
 65 70 75 80
 Gly His Gly Leu Glu Val Glu Ile Asn Cys Thr Arg Thr Gln Asn Thr
 85 90 95
 Lys Cys Arg Cys Lys Pro Asn Phe Phe Cys Asn Ser Thr Val Cys Glu
 100 105 110
 His Cys Asp Pro Cys Thr Lys Cys Glu His Gly Ile Ile Lys Glu Cys
 115 120 125
 Thr Leu Thr Ser Asn Thr Lys Cys Lys Glu Glu Gly Ser Arg Ser Asn
 130 135 140
 Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 145 150 155
